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(54) Title: p-53 BINDING PROTEIN CALLED Mdmx AND ENCODING SEQUENCES FOR SAID PROTEIN

(57) Abstract

The present invention provides a method to identify new proteins associating to the p53 tumor suppressor protein as well as elucidating the genes encoding said proteins, with some examples of cDNAs isolated this way. It also relates to the results of said method, which are novel proteins having affinity for p53, as well as genes and other nucleic acid molecules encoding these novel proteins. In particular the invention also provides such a novel protein and its encoding sequences, which protein has homology with the Mdm2 protein and which therefore has been designated as Mdmx.

P-53 BINDING PROTEIN CALLED MDMX AND ENCODING SEQUENCES FOR SAID PROTEIN

The present invention relates to molecular biology techniques and especially to their application in cancer research. In particular a method to identify new proteins associating to the p53 tumor suppressor protein, with some examples of cDNAs isolated this way is disclosed. It also relates to the results of said method, which are novel proteins having affinity for p53, as well as genes and other nucleic acid molecules encoding these novel proteins.

In particular the invention also relates to one such a novel protein and its encoding sequences, which protein has homology with the Mdm2 protein and which therefor has been designated as Mdmx.

The process by which a normal cell is transformed into a tumorigenic cell that can grow out to form a tumor is a very complex process in which several independent genetic changes have to take place. These genetic alterations can be roughly divided into two classes. The first comprises the genetic changes that alter the abundancy or properties of a gene product in such a way that it constitutively stimulates cell growth. The second class comprises genetic alterations that inhibit the normal cell growth controlling function of a gene product. An important role in the switch from normal cell to tumor cell is assigned to a protein called p53.

The protein called p53 has properties of both classes. Mutations in the p53 gene as found in human tumors abolish the tumor suppressor activity of the protein. In addition, several mutated forms of the p53 protein can have a dominant stimulating effect on cell growth.

Alterations in the p53 coding sequence are observed in over 50% of all human tumors. This makes p53 mutations the most frequent observed alteration in human cancer.

Many functional studies on p53 indicate that alterations in the p53-controlled functions can be very important for the

genesis and progression of a tumor. Mouse model studies show that either overexpression of a mutant p53 gene or inactivation of the normal wild-type p53 gene results in the development of tumors somewhere between the age of 3 and 6 months.

In humans it has been found that an hereditary form of cancer, the Li-Fraumeni Syndrome, is associated with a germ-line mutation in one allele of the p53 gene. In the tumors the remaining wild-type allele has been lost, indicating the importance of loss of wild-type p53 function for carcinogenesis.

One of the ways in which P53 probably functions is by guarding the integrity of the genome of cells. It can do so in two ways, namely through influencing the cell cycle and/or the process of repairing DNA damage and secondly by influencing the apoptosis pathway.

In the event that cells have received a dose of a DNA damaging agent, like ionizing radiation or some chemicals like cisplatin, p53 can arrest the cell in the cell cycle. The p53 protein may also be involved in the repair of the DNA. The presence of DNA damage results in an increase of the p53 protein levels through protein stabilization. Subsequently, the increased levels of p53 result in the activation of transcription of a set of p53-responsive genes. Two of the most important p53-responsive genes identified sofar are the gene coding for an inhibitor of the cyclin-dependent kinases cdc2, cdk2, cdk4 and cdk6, and a gene called gadd45. The cdk-inhibitor is called p21cip1/waf1, and is a member of an expanding family of cdk-inhibitors. These inhibitors inactivate the cdk's by direct binding. The activity of the cdk's, in conjunction with their appropriate cyclin partner, is essential for the progression through the cell cycle. Thus, by increasing the p21cip1/waf1 expression, p53 blocks the cell cycle progression and arrests the cells in the G1 phase mainly. The current hypothesis is that this cell cycle delay allows the cell to repair its DNA before the DNA synthesis starts up and introduces mutations at the sites of the DNA

damage. The second p53-responsive gene important in this respect is the gadd45 gene. It has been shown that (over)expression of gadd45 also blocks cell cycle progression and it has been suggested that gadd45 might have a direct role
5 in stimulating the process of DNA repair.

The second process p53 is involved in that is important for maintaining genomic integrity is apoptosis or programmed cell death. Apoptosis is a very ordered, active process that eventually results in the death of a cell. The process is very
10 important in embryogenesis to get rid of superfluous cells. Recently more and more evidence has accumulated showing that interference with the apoptotic pathways can be very important for a cell to become a tumor cell. In addition, a successfull treatment of tumors might depend on the possibility to induce
15 an apoptotic pathway in the tumor cells. Two *in vivo* studies underscoring the notion that p53 is involved in apoptosis have been most informative. First, it was found that transgenic mice expressing an SV40 largeT mutant which can only bind and inactivate members of the retinoblastoma family(p105^{RB},
20 p107, p130) but which has no effect on p53 function, develop tumors of the choroid plexus epithelium, but only very slowly compared to mice expressing the wild-type T-antigen. However,
the same transgene can induce the development of rapidly
25 growing tumors in p53-deficient mice. Comparison of the slowly growing and rapidly growing tumors revealed that the slowly growing tumors contained a significant percentage of apoptotic cells, which could hardly be found in the rapidly growing tumors. In another mouse model it was found that treatment of tumors lacking any functional p53 with X-rays or adriamycin
30 hardly affected the tumor growth, while tumors containing a wild-type p53 but otherwise comparable could be eradicated. Analysis of both types of tumors after treatment showed the induction of apoptosis in the wild-type p53 containing tumor cells but not in the cells lacking p53. The mechanism by which
35 p53 induces apoptosis has not been completely solved yet. On the one hand, high levels of p53 can lead to induction of expression of a gene called Bax-1 that has been shown to

stimulate apoptosis. On the other hand, a correlation between the induction of p53-dependent apoptosis and transcription repression by p53 has been found. It could be that both activation and repression of transcription by p53 is necessary 5 to get efficient induction of apoptosis. In addition, cell type specificity in the mechanism by which p53 activates apoptosis is well possible.

The above thus gives an indication on the importance of p53 in suppressing tumor activity and possible mechanisms for 10 said suppression. It also gives an indication of the effects of the absence of functional p53 for instance through mutations in the coding region of p53.

Apart from mutations in the coding region of p53, inhibition of the tumor suppressor function of the wild-type 15 p53 can also occur through an altered-cytoplasmic- subcellular localization. The underlying mechanism for this retainment of the protein in the cytoplasm is unknown.

A third way to abolish the p53 tumor suppressor function is through complexation with another cellular protein called 20 Mdm2. The gene encoding this protein was originally isolated from a mouse double-minute present in a spontaneously transformed Balb 3T3 cell line and shown to be responsible for the transformation. Later, it was found that a protein binding to p53 was exactly the same Mdm2 protein. In the transformed 25 cells Mdm2 probably acts by binding to the p53 protein and inactivating its tumor suppressor function. In addition, it has been shown that binding of Mdm2 to p53 completely inhibits the capacity of p53 to activate transcription of a reported 30 gene containing a p53-consensus DNA binding site in its promoter region. Interestingly, the transcription of the mdm2 gene is also stimulated by increased p53 levels. In that way a kind of feedback loop is established between Mdm2 and p53. Functions for Mdm2 apart from the inhibition of p53 activity 35 are not clear. On the one hand an activity as transcription factor has been suggested, both because of its primary protein sequence that shows some Zinc-fingers possibly involved in DNA binding and because the Mdm2 protein has been found to

associate to the TATA-Binding Protein (TBP). This is the first protein to bind to TATA-containing promoters in the assembly of the basic transcription machinery complex. In addition, it has been reported that Mdm2 can effect the function of another 5 transcription factor important in processes related to cancer, E2F-1. The activity of E2F-1 as a transcription factor is normally controlled by another tumor suppressor protein, the product encoded by the retinoblastoma predisposing gene. Active E2F-1 can activate the transcription of genes encoding 10 proteins that stimulate cell growth, like the myc oncogene. Mdm2-overexpression, mainly through amplification of the gene, has been observed in a significant percentage of certain tumor types, establishing a role for this gene in carcinogenesis.

In conclusion, it is clear that a complete elucidation of 15 the p53-controlled pathways and the identification of genes/proteins involved in these pathways can be very beneficial for understanding the onset and/or development of cancer. One way to understand more of p53 functions is to find out whether p53 has other cellular partners apart from Mdm2 20 that affect its tumor suppressor activity. An at this moment very widely used method to identify new proteins associating to a protein of interest is the yeast two-hybrid method. With the use of this method in literature two genes have been described coding for p53-associating proteins. However, the 25 molecular functions of these proteins and their putative involvement in carcinogenesis are unknown as yet. Other methods to identify systematically new p53-associating proteins have not been described in literature.

Thus, it is clear that the development of another way 30 to provide us with genes coding for proteins binding to p53 can be very important for understanding the p53 functions and the process of carcinogenesis. The present invention provides a method to arrive at proteins binding to p53 and the elucidation of their encoding genes.

35 One aspect of the present invention is the application of a method partly known in itself for the isolation of

associating proteins for the identification of (new) p53-
associating gene products.

A first step in the methods according to the invention is
the high level expression of the p53 protein in bacteria, with
5 subsequent purification and radioactive labelling of the p53
protein.

A second step is the use of the labeled p53 protein as a
probe to screen cDNA expression libraries to pick up
associating proteins and subsequently the isolation of the
10 encoding cDNAs.

In a further aspect of the invention the resulting
nucleic acids (such as cDNA's) encoding the novel associating
proteins and the proteins themselves are provided.

15 In figures 2a and 2b partial sequences of novel nucleic acids
encoding such novel proteins are given. Figure 3 gives a novel
cDNA sequence encoding another such novel protein which we
have called Mdmx.

This last one is called Mdmx because of its homology to
Mdm2.

20 The longest cDNA isolated sofar is 1701 nucleotides, and
contains an open reading frame of 489 amino acids, exactly the
same as the mouse mdm2 open reading frame.

The cDNA given in figure 3 is of mouse origin. It will be
clear that using the present invention other mammalian species
25 will be shown to have a counterpart of the Mdmx gene. These
counterparts are of course included in the present invention.
Especially because of the recently developed techniques such
as PCR, it will be within the skilled man's ability to
identify these counterparts and to design functional
30 equivalents and/or fragments of the novel gene and its
products.

It can be seen in fig. 4 that especially the N-terminal
part of the Mdmx protein is very similar with the Mdm2
protein. It has been shown that the N-terminal 100 amino acids
35 in the Mdm/*2 protein are essential for the binding to the p53
protein. This result indicates a certain conservation in p53
binding domains in different proteins, suggesting that other

proteins might contain such a domain as well. Furthermore, a strong conservation of two metal-binding domains in the C-terminal halve of the protein is found. This conservation suggests an important function for this part of the protein,
5 possibly in binding to DNA/RNA or to other proteins.

The third conserved motif is a possible nucleotide binding site (GKT) at amino acid positions 451-453.

(Fig 4; amino acid sequence of the putative Mmdx protein, and a comparison with the mouse and the human Mdm2 protein)

10 All the applications which have and can be envisaged for Mdm2 proteins or their encoding nucleic acids or parts thereof can of course be applied for Mdmx as well.

For instance, it can be envisioned that the Mdmx gene product(s), like the Mdm2 potein, has a role in certain types
15 of cancer. Therefore, the status of the mdmx gene and the expression level can be monitored. This can be performed in several ways. First, the putative overexpression can be a result of gene amplification. This can be investigated by Southern blotting. We have already performed a pilot study to
20 examine possible amplification of the mdmx gene in primary neuroblastomas and in neuroblastoma cell lines. Equal amounts of paired DNAs of normal and tumor tissue from a patient were digested with restriction enzymes, fractionated on a agarose gel, blotted onto nylon membranes and probed with a ³²P-labeled fragment of the human mdmx cDNA.
25

Results so far do not show any indication for amplification of the mdmx gene in neuroblastoma. To be certain a larger panel of tumors and cell lines has to be analyzed.

Another way to investigate overexpression of the gene is
30 by quantitative RT-PCR analysis of the mRNA expression level in the tumors. The primers mentioned earlier that amplify a specific band of human mRNA could be used for this purpose.

The last method to analyze mdmx expression is at the protein level. Antibodies raised against the protein can be
35 used, if necessary after purification, for in situ histochemistry studies on frozen sections or paraffin-embedded tissues. These types of experiments will give both an answer

as to the level and the localization of the protein in the cell.

Since it is not unlikely that Mdmx (over)expression plays a role in the development in (some types of) cancer, it may be 5 important to be able to block Mdmx function in a cell. If the function is to bind and inactivate p53, this interaction could theoretically be relieved by introducing into the cell an overdose of peptide from the Mdmx domain that is necessary for the association to p53. Through competition the binding will 10 be blocked.

Another possibility is to develop mutants of mdmx that can act dominant-negative on the wild-type protein. Possible target domains for mutations are the putative nucleotide binding site and the putative metal-binding motifs. These 15 mutants can be cloned in viral expression vectors (retrovirus, adenovirus, AAV) for delivery to the target cells. It is still possible that MDMX does not inactivate p53, but actually enhances the functions of p53 or is an intermediate in the p53 functional pathways. If that turns out to be the case, not a 20 mutant but a wild-type mdmx gene will be cloned in the expression vectors mentioned above and be delivered to the target cells.

From the comparison between Mdm2 and Mdmx proteins it can be concluded that some of the amino acids in the p53-binding 25 domain are more important than others. We want to use this knowledge to develop primer sets that might amplify other genes containing a p53-binding domain from the same family.

Experimental

30 Cloning of the human wild-type p53 sequence into bacterial expression vector

The coding region for the wild-type human p53 protein was amplified by PCR with primers containing a KpnI site at the 5' end and a SacI site at the 3'-end. After amplification and 35 cutting the fragment with the mentioned restriction enzymes the resulting DNA fragment was cloned into a SacI and KpnI-digested modified version of the pET-15b vector obtained from

Novagen. This modified vector contains 5' of the cloning sites a DNA sequence coding for five aminoacids (RRASV) that is recognized as a phosphorylation site for the Heart Muscle Kinase. Downstream from the cloning sites a sequence coding 5 for 6 histidines is present.

As a result a fusion p53 protein can be synthesized in bacteria, containing at its N-terminal end a peptide stretch with a phosphorylation site for the Heart Muscle Kinase (Sigma) and at its C-terminal end a stretch of six histidines 10 that allows purification over a nickel chelate column (Pharmacia). Figure 1 shows the main features of the p53 expression vector.

Production, purification and radioactive labelling of
15 bacterially produced p53 protein

After construction the plasmid was propagated in the bacterial strain HB101, and subsequently transformed into the E. coli B-strain BL21(DE3) or this strain containing pLysE. The induction of protein expression has essentially been 20 performed according to the pET system manual provided by Novagen. In short, a BL21(DE3) colony containing the p53 expression plasmid was grown at 37°C to OD₆₀₀ of 0.6. IPTG was added to a final concentration of 1mM and incubation was continued for another 3 h. After cooling on ice the cells were 25 harvested by centrifugation at 4°C at 5000 x g for 10 min. Cells were grown for additional four hours and pelleted by centrifugation for 10 min at 5000xg. The pellet was rinsed with ice cold PBS and resuspended in IMAC- 5 (20 mM Tris pH 8, 0.5 M NaCl, 5 mM Imidazole, 10 µg/ml PMSF 30 (phenylmethylsulfonyl fluoride). The bacteria were lysed on ice by sonication (3x30 s.) and centrifuged at 20.000xg for 30 min at 4°C. It turned out that over 90% of the produced p53 protein was retained in the pellet. Bacterial pellet of insoluble proteins including p53 was incubated in IMAC-5 with 35 6 M urea for 30 minutes on ice. After centrifugation for 30 minutes at 30.000xg the urea was removed from the soluble fraction with the use of a 10DG desalting column (Bio-Rad).

The p53 fusion protein was purified using nickel chelate chromatography according to manufacture instructions (Novagen).

The column was washed with increasing concentrations of 5 imidazole (10, 20, 40, 100 and 200 nM). Coomassie staining of a SDS-PAGE gel indicated that the protein eluted at 200 nM imidazole was over 70% pure.

For screening an expression library purified protein was 10 radioactively labeled with the HMK(Sigma) and ^{32}P -ATP according to the manufacturers protocol. Unincorporated radioactive nucleotides were removed with the use of a Sephadex G-25 column equilibrated with PBS/1% non-fatty dry milk. The protein could be labeled to a specific activity of $> 10^7$ cpm per microgram protein.

15

Screening of expression library with radioactive labeled p53 protein

A cDNA library from a 16-day-old mouse embryo was obtained from Novagen. The cDNAs had been cloned into the 20 lambda EXlox vector from Novagen and transformed into the E.coli strain BL21(DE3)pLysE. Approximately 10^6 phages were plated onto 15 150 mm dishes. Dishes were incubated at 37°C for 3-4 hours. When the plaques has become visible, 0.45 μm nitrocellulose filters (Schleicher and Schüll) soaked in 10 mM IPTG were placed over the plaques and proteins were allowed to 25 transfer overnight. Filter hybridization has been performed essentially as described by Ayer et al. (Cell 72, 211-222, 1993). Shortly, the filters were blocked for several hours in HBB/5% NFDM [20 mM HEPES (pH 7.5), 50 mM KCl, 10 mM MgCl₂, 10 mM β -glycerol phosphate, 1 mM DTT, 0.1% NP-40 and 5% non-fatty dry milk]. Hybridization was performed overnight with at 30 least 2×10^5 cpm/ml p53 probe in [20 mM HEPES(pH 7.5), 50 mM KCl, 10 mM MgCl₂, 10 mM β -glycerol phosphate, 10 mM DTT, 0.1% NP-40 and 10% glycerol] at 4°C. After hybridization the 35 filters were washed once in PBS containing 0.2% Triton X-100 for 10 minutes, and three additional washes were done in PBS, 0.2% Triton X-100, 100 mM KCl, for 15-20 minutes at 4°C.

After washing the filters were allowed to air dry, wrapped in Saran wrap and exposed to X-ray films.

Results: isolation of three cDNAs

5

The initial screen yielded 10 possible positive clones. After a second and third round screen, only three positive lambda clones remained. A purified phage preparation was introduced into the E.coli strain BM25.8 (Novagen). Through 10 the Cre-loxP autosubcloning system, plasmids containing the insert are generated. PCR analysis of the three positive clones with the use of primers from the flanking vector sequences showed inserts of approximately 600, 800 and 1700 bp (named clone 1, 2 and 3, respectively). The first two clones 15 were partially sequenced; the DNA sequence obtained showed no significant homology to any known sequence submitted to the several databases. (Fig 2; partial sequence of two smaller clones, clone 1 and clone 2).

The sequence of the third clone showed clear homology 20 with a cloned human gene called mdm2. This is to date the only human gene whose gene product can bind to and inactivate the tumor suppressor function of p53, probably by inhibiting its capacity to activate the transcription from promoters containing a p53-recognition consensus DNA sequence (see 25 above).

This gene was called the mdmx gene.

The expression of the mdmx gene was investigated by Northern blotting. A polyA+ mRNA blot containing RNA isolated 30 from several mouse tissues was hybridized with a complete mdmx cDNA-fragment isolated. In all tissues mRNAs of approx. 10 kb and 8 kb were observed. In addition, in testis two strong hybridizing bands of ~ 2000 bp and 1700 bp were seen. These bands are also presents in other tissues but much less abundant. It is unclear as yet what the origin of the longer 35 mRNAs is. It is thus not excluded that the genomic gene that gives rise to expression of mdmx codes for several, more or less, related proteins that can or cannot bind to p53.

RNA expression of mdmx could also be found by RT-PCR in several mouse tissues and cell lines. Some of the primers from the mouse sequence did also yield a band of expected length with RNA extracted from human cells/cell lines, indicating already the existence of a human homologue of the mdmx gene. This human PCR fragment was cloned and sequenced. The sequence showed high percentage of identity, but not complete, strongly indicating that part of the human homologue was cloned. In addition, screening of a human cDNA library yielded a cDNA that also has a high percentage identity with the mouse mdmx cDNA. In total approximately 750 bp of the probable human homologue of mdmx has been cloned and sequenced.

To obtain antisera recognizing the Mdmx protein three synthetic peptides were coupled to BSA and injected both in rabbits and in mice. We have now obtained one strongly positive polyclonal rabbit antiserum. Mouse sera will be tested and if positive we will try to generate hybridoma's that produce monoclonal antibodies recognizing mdmx protein.

Expression of mdmx cDNA

The mouse mdmx cDNA was cloned into a CMV-driven eukaryotic expression vector. Transfection of this construct into human or mouse cells yielded the production of an approximately 65 kDa protein as determined by Western blotting on total cell lysates and detection of the protein with a polyclonal rabbit antiserum. (The apparent size of the protein is less than expected based on the homology with mdm2; this runs at approximately 90 kDa; the theoretical molecular weight of both proteins is about 55 kDa. It is not known yet whether the smaller size is an artifact of the expression vector -some mutation?, although we sequenced the expression vector- or that 65 kDa is the real Mr. The fact that the human mdmx protein runs at ~80 kDa on the same type of gel -see below- makes us hesitant about the mouse protein size).

The same expression vector was used to investigate the effect of mdmx expression on transcriptional transactivation by wild-type p53. We found that cotransfection of mdmx could inhibit the transcription activation by wild-type p53, like mdm2. Furthermore, the inhibition by mdmx was mapped to the transcription activation domain of p53 (N-terminal domain). This is the p53 domain to which it was shown that mdm2 binds, suggesting that mdmx also will bind to this part of p53.

Two mouse genomic clones have been isolated from a 129/Ola mouse library. One of these contained the 5' end of the 'cDNA' sequences. To investigate whether upstream sequences contained promoter activity, parts were cloned in front of the luciferase reporter gene. It turned out that 1 kb of upstream sequence is sufficient to obtain full promoter activity. The promoter activity is rather high in this assay, comparable to the RSV Long Terminal Repeat. These results suggest that at least one of the mdmx promoters is located in this region.

Characterization of the same genomic clone indicated a difference in organization compared to mdm2. The mdmx homologues of the sequences that are found in the first three exons of the mdm2 gene. This also means that the p53-responsive element located in the first intron of mdm2 is not

present, at least not in the same position, in the mdmx gene (Fig. 8). The absence of a p53-responsiveness is supported by an experiment showing that mdm2 gene expression is p53-dependently increased after UV-irradiation but that mdmx expression is not increased by the same treatment. This result suggests a different regulation of expression of the mdm2 and mdmx genes.

Isolation of human MDMX cDNA (hMDMX)

With the use of the mouse cDNA as a probe, a human cDNA-library from T84 colonic epithelial cells was screened to obtain a human cDNA encoding the MDMX protein. Two partial cDNAs were obtained, from which the nucleotide sequence was determined. In Fig. 5 the combined sequence is depicted of the hMDMX cDNA obtained so far. In Fig. 6 a comparison at the protein level between MDMX and hMDMX is shown. In Fig. 7 a comparison between the amino acid sequences of human MDM2 and human MDMX is shown.

The full length coding region of human MDMX was cloned into the modified pET15b vector, described earlier for the production of human p53, and transformed into E. coli BL21. Production of human MDMX protein was induced by the addition of IPTG, cells were harvested and total lysates separated on a polyacrylamide-SDS gel. A protein of approximately 80 kDa was clearly induced upon addition of IPTG. After purification on a nickel-chelate column the protein was injected into rabbits for the production of an antiserum recognizing the human MDMX.

The His-tag in the MDMX-construct in the pET15b expression vector was also replaced by an HA-tag (HA=haemagglutinin). Production of the 'same' 80 kDa protein could now be detected after Western blotting and immunoincubations with the anti-HA antibody.

In addition, the full length coding region for human MDMX was cloned into pcDNA3 vector (Invitrogen). With the use of a coupled in vitro transcription/translation kit (Promega) a ^{35}S -labelled protein was produced of approximately 8-kDa. After incubation with bacterially produced human p53 protein

followed by an anti-p53 immunoprecipitation, this protein was specifically co-precipitated, indicating the binding between human MDMX and human p53. In the same expression vector an HA-tag was added at the carboxy-terminal end of the protein.

- 5 After transfection into COS-1 cells a protein of approximately 80 kDa could be detected by Western blotting with the use of the commercially available anti HA-tag antibody.

An internal fragment of the human MDMX cDNA was used as a probe to screen a human P1 genomic library constructed from 10 normal human fibroblast cells (Reference Library - Catabase, Max-Planck-Institut for Molecular Genetics, Berlin-Dahlem, Germany). Finally one P1 clone was purified containing human MDMX sequences. This P1 clone was used for chromosomal localization by FISH. The human MDMX gene was found to 15 localize to human chromosome 1q32. Amplification of this region has been found in some liposarcomas (Forus et al., Genes Chromosomes and Cancer 14, 8-14 (1995); Szymanska et al., Genes Chromosomes and Cancer 15, 89-94 (1996), which might imply a role for MDMX in the genesis of these tumors.

CLAIMS

1. A recombinant or isolated nucleic acid molecule encoding at least a biologically functional part of a mammalian protein capable of binding to a p53 protein and comprising at least a part of the sequence

5	1	GTGGCTCTTG	CGAACTCTGG	GTTTGAGAGG	CCGGAACCTGG	TGCTGCCGTT
	51	GCTCGCAGTT	TCAAAATGCA	GTGCAGGCCT	TAGGGTCTCC	GGCTGCCACC
	101	CCTCCCCCAG	CTAGGAGGGG	GAGCGACTCA	TGGAGCggcc	GTAAGTTTGC
	151	TAACTGTGGA	GTCTTCACTG	CCAAAATGAC	ATCACATTCC	ACCTCGGCC
10	201	AGTGTTCAGC	ATCTGACAGT	GCTTGCAGAA	TTTCTTCGGA	ACAAATTAGT
	251	CAGGTGCGGC	CAAAACTGCA	GCTTTGAAAG	ATTTTGCATG	CAGCAGGTGC
	301	GCAGGGGGAA	GTATTCCACCA	TGAAAGAGGT	AATGCACTAT	CTAGGCCAGT
	351	ATATAATGGT	GAAGCAGCTC	TATGATCAAC	AGGAGCAACA	TATGGTATAC
	401	TGTGGTGGAG	ATCTTTGGG	AGATCTACTT	GGATGTCAGA	GCTTTTCTGT
15	451	GAAAGATCCA	AGCCCTCTCT	ATGACATGCT	AAGAAAGAAT	CTTGTACAT
	501	CAGCTTCTAA	TAACACAGAT	GCTGCTCAGA	CTCTCGCTCT	CGCACAGGAT
	551	CACACTATGG	ATTTTCCAAG	TCAAGACCGA	CTGAAGCACG	GTGCAACAGA
	601	ATACTCCAAT	CCCAGAAAAA	GAACGTAAAGA	AGAGGATACT	CACACACTGC
	651	CTACCTCACG	ACATAAATGC	AGAGACTCCA	GAGCAGATGA	AGACTTGATA
20	701	GAACATTTAT	CTCAAGATGA	GACATCTAGG	CTTGACCTTG	ATTTTGAGGA
	751	GTGGGACGTT	GCTGGCCTGC	CTTGGTGGTT	TCTAGGAAAT	TTGAGAAACA
	801	ACTGTATTCC	TAAAAGTAAT	GGCTCAACTG	ATTTACAGAC	AAATCAGGAT
	851	ATAGGTACTG	CCATTGTTTC	AGACACTACG	GATGATTGTT	GGTTTTTAAA
	901	TGAGACCGTG	TCAGAGCAAT	TAGGTGTTGG	AATAAAAGTT	GAAGCTGCTA
25	951	ATTCTGAGCA	AACAAGTGAA	GTAGGGAAAA	CAAGTAACAA	GAAGACGGTG
	1001	GAGGTGGGAA	AGGATGATGA	TCTTGAGGAC	TCCAGGTCTC	TGagCGATGA
	1051	TACTGACGTG	GAACTTACCT	CTGAGGATGA	GTGGCAGTGT	ACGGAATGCA
	1101	AGAAAGTTAA	TTCTCCAAGC	AAGAGGTACT	GTTTTCGTTG	CTGGGCCTTG
	1151	AGAAAAGGATT	GGTATTGGA	TTGTTCTAAA	TTAACCTCATT	CCCTATCTAC
30	1201	ATCTAATATT	ACTGCCATAC	CTGAAAAGAA	GGACAATGAA	GGAATTGATG
	1251	TTCCCGATTG	TAGGAGAACCC	ATTTCAAGCTC	CTGTTGTTAG	GCCTAAAGAT
	1301	GGATATTAA	AGGAGGAAAA	GCCCAGGTTT	GACCCTTGCA	ACTCAGTGGG
	1351	ATTTTTGGAT	TTGGCTCATA	GTTCTGAAAG	CCAGGAGATC	ATCTCAAGCG
	1401	CGAGAGAACAA	AACAGATATT	TTTTCTGAGC	AGAAAAGCTGA	AACAGAAAGT
35	1451	ATGGAAGATT	TCCAGAATGT	CTTGAAGCCG	TGTAGCTTAT	GTGAAAAAAG
	1501	GCCTCGGGAT	GGGAACATTA	TTCATGGGAA	GACGAGCCAT	CTGACGACAT
	1551	GTTCCTACTG	TGCCAGGAGA	CTGAAGAAGT	CTGGGGCTTC	GTGTCCTGTT
	1601	TGTAAGAAAG	AGATTCAAGT	GGTTATTAAA	GTTTTTATAG	CATAGTTGAG
	1651	TCAGTCACAG	AGAAATACTA	GGAGGACCAG	GTCATTATC	AAAAAAAAAA
40	1701	A				

or a functional equivalent thereof.

2. A nucleic acid molecule according to claim 1 which is a cDNA.

3. A nucleic acid molecule according to claim 1 or 2, encoding at least a functional part of the human equivalent of the sequence of claim 1.
4. A recombinant vector comprising a nucleic acid molecule according to claims 1-3 together with suitable elements for regulation of replication and/or expression.
5. A recombinant host cell comprising a vector or a nucleic acid molecule according to anyone of the foregoing claims.
6. An isolated or recombinant proteinaceous substance comprising at least a biologically functional part of an amino acid sequence resulting from the translation of a nucleic acid molecule according to any one of claims 1-3, the expression of a vector according to claim 4 and/or the culture of a cell according to claim 5.
- 15 7. A method for the identification of proteins having a binding affinity for p53 comprising the steps of labelling a proteinaceous substance comprising at least the binding site of a p53 protein and hybridizing said substance with the protein to be tested.
- 20 8. A method for the identification of nucleic acid molecules encoding proteins having a binding affinity for a p53 protein comprising the steps of expressing said nucleic acid in a suitable expression system, labelling a proteinaceous substance comprising at least the binding site of a p53 protein and hybridizing said substance with the protein to be tested.
- 25

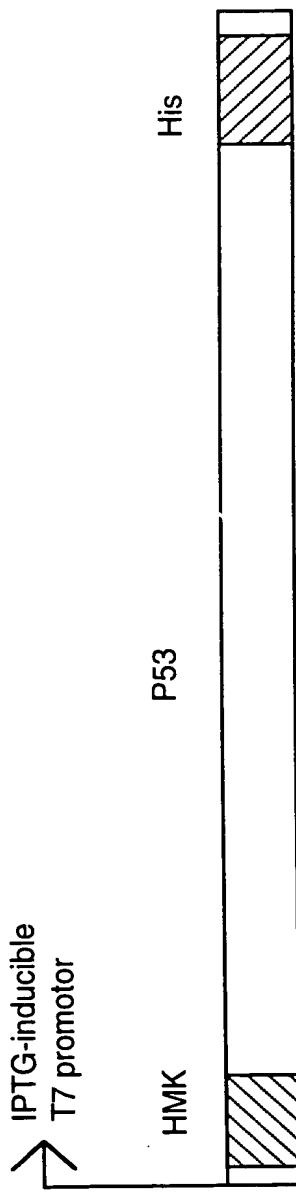


FIG. 1 Schematic representation of the bacterial p53-expression vector

Fig. 2 Partial sequence of clone 1 and clone 2

A. Clone 1

GTATGAGGTGGAAGAACAGAAGTGGTCATNAAGTCATACCA
5 GGATGVNNGHAGACAAAAAGAA----- ~400 bp -----GTATGAGGTGGAAGAACAGAAGTGGTCATNAAGTCATACCA
GGATGVNNGHAGACAAAAAGAAAGCTTGGNNCTATTCTATAGTGT
10 CACCTAAAGACT

AGCTTG

B. Clone 2

CCTTCCGTTGAGGTATGTAGTACCCACTGATACCAGTATTG
15 TAATGACAGACACTGC

TTTCTCTGAGGGGAAGTCTGTTCATTTGCACATTCCGTTGTAAA

-----600 bp---CACCAACCACACKCACARACACACKCCC
15 AACAAACAAAAAAGCTTGGGCCT

A: Adenosine

R: A or G

K: G or T

C: Cytidine

Y: C or T

N: A, C, G or T

20 G: Guanosine

V: A, C or G

T: Thymidine

H: A, C or T

Fig. 3 DNA sequence of the mouse mdmx cDNA

1	GTTGGCTCTTG	CGAACTCTGG	GTTTGAGAGG	CCGGAACTGG	TGCTGCCGTT	
51	GCTCGCAGTT	TCAAAATGCA	GTGCAGGCCT	TAGGGTCTCC	GGCTGCCACC	
101	CCTCCCCCAG	CTAGGAGGGG	GAGCGACTCA	TGGAGCGGCC	GTAAGTTGC	
5	151	TAACTGTGGA	GTCCTCACTG	CCAAAATGAC	ATCACATTCC	ACCTCGGCC
201	AGTGTTCAGC	ATCTGACAGT	GCTTGCAGAA	TTTCTTCGGA	ACAAATTAGT	
251	CAGGTGCGGC	CAAAAATGCA	GCTTTGAAG	ATTTTGCATG	CAGCAGGTGC	
301	GCAGGGGGAA	GTATTACCCA	TGAAAGAGGT	AATGCACTAT	CTAGGCCAGT	
351	ATATAATGGT	GAAGCAGCTC	TATGATCAAC	AGGAGCAACA	TATGGTATAC	
10	401	TGTGGTGGAG	ATCTTTGGG	AGATCTACTT	GGATGTCAGA	GCTTTCTGT
451	GAAAGATCCA	AGCCCTCTCT	ATGACATGCT	AAGAAAAGAT	CTTGTACAT	
501	CAGCTTCTAA	TAACACAGAT	GCTGCTCAGA	CTCTCGCTCT	CGCACAGGAT	
551	CACACTATGG	ATTTTCCAAG	TCAAGACCGA	CTGAAGCACG	GTGCAACAGA	
601	ATACTCCAAT	CCCAGAAAAA	GAACTGAAGA	AGAGGATACT	CACACACTGC	
15	651	CTACCTCACG	ACATAAATGC	AGAGACTCCA	GAGCAGATGA	AGACTTGATA
701	GAACATTAT	CTCAAGATGA	GACATCTAGG	CTTGACCTTG	ATTTTGAGGA	
751	GTGGGACGTT	GCTGGCCTGC	CTTGGTGGTT	TCTAGGGAAT	TTGAGAAACA	
801	ACTGTATTCC	TAAAAGTAAT	GGCTCAACTG	ATTTACAGAC	AAATCAGGAT	
851	ATAGGTACTG	CCATTGTTTC	AGACACTACG	GATGATTGT	GGTTTTAAA	
20	901	TGAGACCGTG	TCAGAGCAAT	TAGGTGTTGG	AATAAAAGTT	GAAGCTGCTA
951	ATTCTGAGCA	AACAAGTGAA	GTAGGGAAAA	CAAGTAACAA	GAAGACGGTG	
1001	GAGGTGGAA	AGGATGATGA	TCTTGAGGAC	TCCAGGTCT	TGagCGATGA	
1051	TACTGACGTG	GAACTTACCT	CTGAGGATGA	GTGGCAGTGT	ACGGAATGCA	
1101	AGAAGTTAA	TTCTCCAAGC	AAGAGGTACT	GTTCAGTTG	CTGGGCCTTG	
25	1151	AGAAAGGATT	GGTATTCGGA	TTGTTCTAAA	TTAACTCATT	CCCTATCTAC
1201	ATCTAATATT	ACTGCCATAC	CTGAAAAGAA	GGACAATGAA	GGAATTGATG	
1251	TTCCCGATTG	TAGGAGAACCC	ATTTCAGCTC	CTGTTGTTAG	GCCTAAAGAT	
1301	GGATATTAA	AGGAGGAAAA	GCCCAGGTTT	GACCCTTGCA	ACTCAGTGGG	
1351	ATTTTGGAT	TTGGCTCATA	GTTCTGAAAG	CCAGGAGATC	ATCTCAAGCG	
30	1401	CGAGAGAACAA	AACAGATATT	TTTCTGAGC	AGAAAGCTGA	AACAGAAAGT
1451	ATGGAAGATT	TCCAGAATGT	CTTGAAGCCG	TGTAGCTTAT	GTGAAAAAAAG	
1501	GCCTCGGGAT	GGGAACATTA	TTCATGGAA	GACGAGCCAT	CTGACGACAT	
1551	GTTTCCACTG	TGCCAGGAGA	CTGAAGAAGT	CTGGGGCTTC	GTGTCCTGTT	
1601	TGTAAGAAAG	AGATTCAAGT	GGTTATTAAA	GTTTTTATAG	CATAGTTGAG	
35	1651	TCAGTCACAG	AGAAATACTA	GGAGGACCAG	GTCATTATC	AAAAAAAAAA
	1701	A				

Fig 4. Amino acid sequence of the putative mouse MDMX protein, and the alignment with the amino acid sequence of mouse MDM2 protein

| = identical amino acid

: = conserved amino acid

The p53-binding domain is depicted in Bold/Italic

The Zinc-finger motif around position 310-320 and the putative Ring finger around position 435-480 are indicated in Bold

The putative nucleotide binding site (451-453) is underlined

	10	20	30	40	50	59
Mdmx	MTSHSTSAQCSASDSACRI- SSEQISQVRPKLQLLKILHAAGAQGEVFTMKEVMHYLGQY					
	: : : : :: : : :: : : : : : : : : : :					
Mdm2	MCNTNMSVSTEGAASTSQIPASEQETLVRPKPLLLKLLKSVGQAQNNDTYTMKEIIIFYIGQY					
	10	20	30	40	50	60
Mdmx	60	70	80	90	100	110
	IMVKQLYDQQEQHMVYCGGDLLGDLGCQSFVKDPSPLYDMLRKNLV	TSASNNTDAAQ				119
	: : : : : : : : : : : : : : : : :					
Mdm2	IMTKRLYDEKQQHIVYCSNDLLGDFGVGVPSFSVKEHRKIYAMIYRNLV	--AVSQQDSGTS				
	70	80	90	100	110	
Mdmx	120	130	140	150	160	179
	LALAQDHMTDFPSQDRKLHGATEYSNPRKRTEEEEDTHTLPTSRHKCRDSRADEDLIEHLS					
	: : : : : : : : : : : : : : : : : : : : :					
Mdm2	LSESRRQP--EGGSDLK-DPLQAPPEEKPSSSDLISRLSTSSRR-RSISETEENTDELP					
	120	130	140	150	160	170
Mdmx	180	190	200	210	220	230
	--QDETSRLDDDFE-EWDVAGLPWWFLGNLRNNCIPKSNGSTDQLQTNDIGTAIVSDTTD					
	: : : : : : : : : : : : : : : : : :					
Mdm2	GERHRKRRRSLSFDPSLGLCELREMCSGG-TSSSSSSSESTETPSHQDLDDGVSEHSGD					
	180	190	200	210	220	230
Mdmx	240	250	260	270	280	290
	DLWFLNETVSEQLVGIGKVEANSEQ--TSEVGKTSNKKTVEVGKDDDLEDSRSLSD--D					
	: : : : : : : : : : : : : : : : :					
Mdm2	CL--DQDSVSDQFSVEFEVESLDSEDYSLSDEGHELSDEDDEVYRVTVYQTGESDTSFE					
	240	250	260	270	280	290
Mdmx	300	310	320	330	340	350
	TDVELTSEDEWQCCTECKKFNSPSKRYCFRCWALRKDWYSDCSKLTHSLSTSNIATAPEK-					
	: : : : : : : : : : : : : : : :					
Mdm2	GDPEISLADYWKCTSCNEMNPLPSHCKRCWTLRENWLPD-DKGDKDKEVISEKAKLENSA					
	300	310	320	330	340	350
Mdmx	360	370	380	390	400	410
	KDNEGIDVPDCRRTISAPVVRPKDGYLKEEKPRFDPCNSVGFLDLAHSSESQEIISSARE					
	: : : : : : : : : : : : : : : :					
Mdm2	QAEGLDVPDGKKLTENDAKEPCAEDSEEKAEQTP-LSQESDDYSQPSTSSIVYSSQE					
	350	360	370	380	390	400

	420	430	440	450	460
Mdmx	QTDIFSEQKAE-TESME-DFQ-NVLKPCSLCEKRPRDGNIIH <u>GKTSHLTTCFH</u> CARRLK :: :: ::: : : : :: : : : : : : : :				
Mdm2	SVKELKEETQHKDESVESSFSLNAIEPCVICQGRPKNGCIVHGKTGHLMSCFTCAKKLKK 410 420 430 440 450 460				
	470	480	490		
Mdmx	SGASCPVCKKEIQLVIKFIA :: : : : : : :				
Mdm2	RNKPCPVCRQPIQMIVLSYFN 470 480				

Fig. 5. Nucleotide sequence of the human MDMX cDNA isolated sofar.

AATTGGCACGAGCTAGGATCTGTGACTGCCACCCCTCCCCCACCAGGGCTGGCGGGGGAGCG
ACTCATGGAGCTGCCGTAAGTTTACCAACAGACTGCAGTTCTCACTACCAAAATGACATCA
TTTCCACCTCTGCTCAGTGTCAACATCTGACAGTGCTGCAGGATCTCTCCTGGACAAATCAAT
CAGGTACGACCAAAACTGCCGTTTGAAGATTTGCATGCAGCAGGTGCGCAAGGTGAAATGTT
CACTGTTAAAGAGGTCACTGACTAATTTAGGTCACTACATAATGGTGAAGCAACTTATGATCAG
C .GGAGCAGCATATGGTATATTGTGGTGGAGATCTTGGGAGAACTACTGGGACGTCAGAGC
TTCTCCGTAAGAACCCAAGCCCTCTCTATGATATGCTAAGAAAAGAATCTTGTCACTTAGCCACT
GCTACTACAGATGCTGCTCAGACTCTCGCTCGCACAGGATCACAGTATGGATATTCCAAGTC
AAGACCAACTGAAGCAAAGTGCAGAGGAAAGTCCACTTCCAGAAAAAGAACTACAGAACGAGATA
TCCCCACACTGCCAACCTCAGAGCATAATGCATACATTCTAGAGAAGATGAAGACTTAATTGAAA
TTTAGCCCAGATGAAACATCTAGGCTGGACCTTGGATTGAGGAGTGGGATGTAGCTGGCCTGCC
TTGGTGGTTTTAGGAAACTTGAGAAGCAACTATACACCTAGAAGTAATGGCTCAACTGATTACA
GACAAATCAGGATGTGGTACTGCCATTGTTCAGATACTACAGATGACTTGTGGTTTTGAAT
GAGTCAGTATCAGAGCAGTTAGGTGTAATAAAGTTGAAGCTGCTGATACTGAACAAACAAGT
GAAGAAGTAGGGAAAGTAAGTGACAAAAGGTGATTGAAGTGGGAAAAATGATGACCTGGAGG
ACTCTAAGTCCTTAAGTGTGATGATACCGATGTAGAGGTTACCTGAGGATGAGTGGCAGTGTAC
TGAATGCAAGAAATTAACTCTCCAAGCAAGAGGTTACTGTTTCTGTTGGCCTTGAGGAAGG
ATTGGTATTCAAGTTCAAAGTTAACCAATTCTCTCCACGTCTGATATCACTGCCACACT
GAAAAGGAAATGAAGGAAATGATGTCCTGATTGTCGAAGAACCATTCGGCTCTGCGTTAG
ACCTAAAGATGCGTATATAAAGAAAGAAAATCCAAACTTTTGATCCCTGCAACTCAGTGGAAATT
CTTGGATTGGCTCACAGTTGAAAGCCAAGAGACCACATCTCAAGCATGGGAGAACAGTTAGATAA
CCTTCTGAACAGAGAACAGATACAGAAAACATGGAGGATTGCCAGAATCTCTGAAGCCATGTA
GCTTATGTGAGAAAAGACCACGGAGACGGAACATTATTCTGAAAGGACGGCCATCTGTCACTT
GTTTCACTGTGCCAGAACAGACTAAAGAAGGCTGGGCTCATGCCCTATTGCAAGAAAGAGATT
CAGCTGGTTATTAAAGGTTTATAGCATATGGTAGTACGAACATAAAATGCATTATTAGTT
CACTTACACATTATTGAAAATCAATCCTTATTAAATTGATCCAACTGTCAGAGAATG
TTCTTAGGCATCAAATCCAAGGTAGCTGTAAGAAAATCTGGAGCTAACATGAAGAACAGAAG
TAATCTGATTAGTCAAATTATAAGTGCATGGATTACTTATGCAGCAGTCAGGTACATAGTT
AGGTGAACCAAAAGAAAAACTCTGAAAACAAGAGATTCTCCATGCACATTACAATATTGAGG
TATAATTAAACATGATAAAAGTGTCTCTAAGGTTGAGAAATCTGAGTAACCACCCAAAAAA
GCAATAGAATGTTGTGTCACCCAAAACACTCCCTCTGCCCTTCTCAGACAGTCCTCAGCTA
TTTCATGGCTCTCACCCCTAGTTTTTTTGTCACTTTTTTCCGGGGTATAGGGG
AGGTGTGGGCGACAGGTCTGCTTGTCTGCTCCAGGCTGAAGTGCAGTGAGTCAAGATT
GAGCCACTGCACTCCAGCCTGGTGACAGCGCAGACTCCATCTCAGAAAAAAAAAAAAAA
AAAAAAACTAT

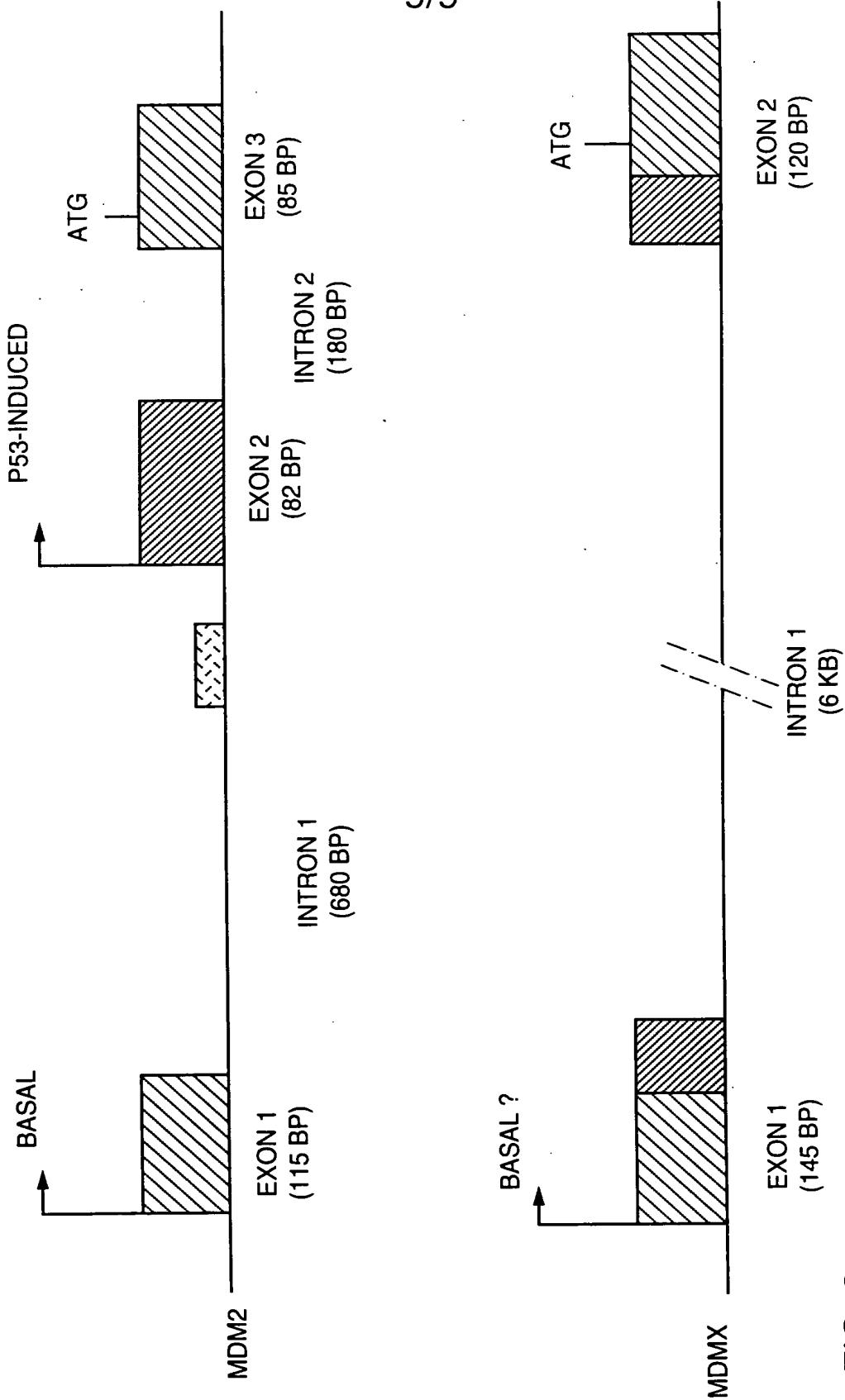
Fig. 6 Comparison of the amino acid sequences of human MDMX and mouse MDMX.
Each protein consists of 489 amino acids.

nMDMX	NTSFSTSAQCSTSDSACRISPGQINQVRPKPLILKILHAAGAQGEMFTYKEVMMHYLGQYIMVK
mMDMX	MTSHSTSQAQCSDSACRISSEQISQVRPKLQLLKILHAAGAQGEVFTMKEVMMHYLGQYIMVK
hMDMX	QLYDQQEQQHMVYQCGDLGLGELLGROSFSVKNPSPYDMLRKNLVTLATATTDAQTLALAQDH
mMDMX	QLYDQQEQQHMVYQCGDLGLGCQSFSVKDPSPLYDMLRKNLVTSAGNNTDAQTLALAQDH
hMDMX	SMDIPSQDLIKQSAEESSTSRKRRTEDDIPIPTSEHKCIHSREDEDLILENLAQDETSRLD LG
mMDMX	TMDFPSPQRDRKLKHGATEYSNPKRRTEDDIPIPTSEHKCIHSREDEDLIEHLSQDETSRLD LD
hMDMX	FEEWDVAGLPWWFLGNLRSNYTPRSNGCSTDLOTNOPOVGTAVISDFTDDLFWFLNEVSFQLGVG
mMDMX	FEEWDVAGLPWWFLGNLRSNCIPKSNGSTDQTNODIGTAIVSFTDDLFNETVSEQLGVG
hMDMX	IKVEAADTEQTSEEYGKVSDKKVIEVGKNDPLESKSLSDDTDVETSEDEWOCTECKKFNSP
mMDMX	IKVEAANSEQTSE. VGGTKTSNKKTVEVGKDQDLEDSSRLSDDTDVELTSEDEWOCTECKKFNSP
hMDMX	SKRYCFRCWALRKDWYSDCSKLTSLSTSDITAIP.E.KENEGNDVPDCRTTISAPVVRPKDAY
mMDMX	SKRYCFRCWALRKDWYSDCSKLTSLSTSNITAIPEKDNEGIDVPCRTTISAPVVRPKDGY
hMDMX	IKKENNSKLFNPQNSYEFPLAHSSESQETISSMGEQLDNLSEQRTDTENMEDCQNLKPCSLC
mMDMX	LKEEKPR.FDPCNISVGFLLAHSSESQELIASSAREQTDIFSEQRAETESMEDFQNVLKPCSLC
hMDMX	EKRPRPGNIIHGRIGHLVTCHCARRLKAGASCPICKKEIQLVIVKVFIA *
mMDMX	EKRPRDGNIIHGKTSHLTTCFHCARRLKSGASCIVCCKKEIQLVIVKVFIA *

Fig. 7 Comparison of the amino acids sequences of human MDM2 and human MDMX.

hMDM2	MCNTNM.SVPTDGAVTTSQIP..AS.EQETLVRPKPLLLKLLKSVGAOKDTYT
hMDMXMTSFSTSAQCSTSDSACRISPGQINQVRPKLPLLKILHAAGAQGEMFT
hMDM2	MKEVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTM
hMDMX	VKEVIHYLGQYIMVKQLYDQQEQQHMVYCGGDLLGELLGQSFVKNPSPPLYDM
hMDM2	IYRNLLVVVNQQESSDSGTSVSENRCLEGGSQKDLVQELQEEKPSSSHL..
hMDMX	LRKNLVTLATATTDAATLALAQDHMDIPS.QDQLKQSAEESSTSRSRKRTTE
hMDM2	..VSRPSTSSRRRAISETEENSDELSGERQRKRHKSDSISLSFDE.....S
hMDMX	DDIPTLPTSEHKCIHSREDEDLIENLAQDETSR.....LDLGFEEDVAGLPW
hMDM2	LALCVIREICCERSSSSESTGTPSNPDLDAGVSEHSGD..WLDQDSVSQFSV
hMDMX	WFLGNLRSNYTPRSNG..STDLQTNQDVGTIAVSDTDDLWFNLNESVSEQLGV
hMDM2	EFEVESLDSEDSLSEEQELSDEDDEYYQVTVYQA.GESDTDSDFEEDPEISL
hMDMX	GIKVEAADTEQ..TSEEVGV..DKKVIEVGKNDLLEDSKSLSDDTDVEVTS
hMDM2	ADYWKTSCNEMNPPLPSHCNRCWALRENWLPEDKGKDGEISEKAKLENSTQ
hMDMX	EDEWQCTECKKFNSPSKRYCFRCWALRKDWYS.DCSKLTHSLSTSITAPEK
hMDM2	AEEGFDPDCKKTI...VNDSCRESCVEENDDKITQASQSQESEDYSQPSTSSS
hMDMX	ENEGLNDVPDCRRTISAPVVRPKDAYIKKENSKLFNPCNSVEFLDLAHSSESQE
hMDM2	IIYSSQEDVKEF..EREETQDKEESVESSLPLNAIEPCVICQGRPKNGCIVHG
hMDMX	TISSMGEOQLNLSEQRTDTENMEDC.....QNLKPCSLCEKPRDGNIHG
hMDM2	KTGHLMACFTCAKKLKRNKPCPVCRQPIQMIVLTYFP *
hMDMX	RTGHLVTCFHCARRLKKAGASCPICKKEIQLVIKFIA *

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**FIG. 8**

INTERNATIONAL SEARCH REPORT

International Application No

PCT/NL 96/00239

A. CLASSIFICATION OF SUBJECT MATTER
 IPC 6 C12N15/12 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
 IPC 6 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO,A,94 08241 (DEUTSCHES KREBSFORSCH ;ZENTGRAF HANSWALTER (DE); SCHRANZ PETER (DE) 14 April 1994 see the whole document ---	7
Y	WO,A,93 20238 (UNIV JOHNS HOPKINS) 14 October 1993 see examples 1,2 ---	8
Y	PROC. NATL. ACAD. SCI. U. S. A. (1987), 84(9), 3038-42 CODEN: PNASA6;ISSN: 0027-8424, XP002013820 SIKELA, JAMES M. ET AL: "Screening an expression library with a ligand probe: isolation and sequence of a cDNA corresponding to a brain calmodulin-binding protein" see the whole document -----	8

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Date of the actual completion of the international search

Date of mailing of the international search report

19 September 1996

15. 11. 96

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Gurdjian, D

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/NL 96/00239

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		AU-A-	4278893	08-11-93
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		EP-A-	0635068	25-01-95
		JP-T-	7505294	15-06-95
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		US-A-	5550023	27-08-96
		US-A-	5519118	21-05-96
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